



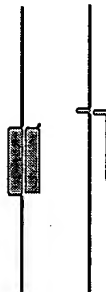
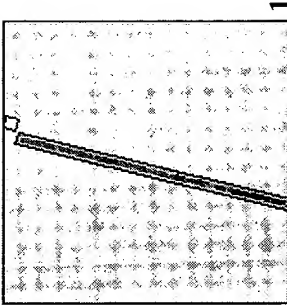
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: ☐ Filter ☒ Align

Sequence 1 lc|seq_1 Length 8509 (1 .. 8509)
Sequence 2 lc|seq_2 Length 2112 (1 .. 2112)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3857 bits (2006), Expect = 0.0
Identities = 2006/2006 (100%)
Strand = Plus / Plus



Query: 2955 ggcaatgggtcgaaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 3014
Sbjct: 1 ggcaatgggtcgaaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 60
Query: 3015 ctgcgcggagagatctctgtgtctcaggtagggcgacaaatggagaggtgttagttgccccctg 3074

|||||
Sbjct: 61 ctgcgcggagatctctggtctcaggtaggcgacaaatggagagggtgtagttgccccctg 120

Query: 3075 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatattccgctagag 3134
|||||
Sbjct: 121 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatattccgctagag 180

Query: 3135 gattactgatagtttctgcctgtcgggcttgcggcttgcgggcttgcgggcttgtc 3194
|||||
Sbjct: 181 gattactgatagtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 240

Query: 3195 gggcctgtccctcttctgtcccgctgtcctcactttttcacaaatcaaaaaatgggcgaagc 3254
|||||
Sbjct: 241 gggcctgtccctcttctgtcccgctgtcctcactttttcacaaatcaaaaaatgggcgaagc 300

Query: 3255 ccttctgttctatagttcttatagtttcattacacgaaaaattacacataattatcaatagctt 3314
|||||
Sbjct: 301 ccttctgttctatagttcttatagtttcattacacgaaaaattacacataattatcaatagctt 360

Query: 3315 attcgcttaaaaggaggagtaattggcgccgcaaaaggagtaattggcgcaaaaggaggt 3374
|||||
Sbjct: 361 attcgcttaaaaggaggagtaattggcgccgcaaaaggagtaattggcgcaaaaggaggt 420

Query: 3375 aattggcgccgcaaaaggaggagtaattggcgccgatatcgggtgtttacatggggagggaatcc 3434
|||||
Sbjct: 421 aattggcgccgcaaaaggaggagtaattggcgccgatatcgggtgtttacatggggagggaatcc 480

Query: 3435 ccttaatcatttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 3494
|||||
Sbjct: 481 ccttaatcatttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 540

Query: 3495 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgcgcaatccgccc 3554
|||||
Sbjct: 541 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgcgcaatccgccc 600

Query: 3555 cgcctgcaggcgctcaagctcatgcatttaatatagaccactgcgggcgcgcgatggct 3614
|||||
Sbjct: 601 cgcctgcaggcgctcaagctcatgcatttaatatagaccactgcgggcgcgcgatggct 660

Query: 3615 gatgatgtgcgcccatgaaatcgggctggccgacattcgcgcaatcgcgcgatgaaaaac 3674
|||||
Sbjct: 661 gatgatgtgcgcccatgaaatcgggctggccgacattcgcgcaatcgcgcgatgaaaaac 720

Query: 3675 catgaccgtgagagcctgaccccgctgttcgaggagctagccgctgcgggtgttgacccat 3734
|||||
Sbjct: 721 catgaccgtgagagcctgaccccgctgttcgaggagctagccgctgcgggtgttgacccat 780

Query: 3735 gatgaccctgcaaaagatgacgtgacagtcggcggttggtcgatgaggcgcgaaatagac 3794
|||||
Sbjct: 781 gatgaccctgcaaaagatgacgtgacagtcggcggttggtcgatgaggcgcgaaatagac 840

Query: 3795 taccgccaggaggcaagcgcggaactcctagtacgtggacctccggaggtacattccgt 3854
|||||
Sbjct: 841 taccgccaggaggcaagcgcggaactcctagtacgtggacctccggaggtacattccgt 900

Query: 3855 cgtatggcggcggtcgaaccactggccattctcgacctcaaacgggtattccatctc 3914
|||||
Sbjct: 901 cgtatggcggcggtcgaaccactggccattctcgacctcaaacgggtattccatctc 960

Query: 3915 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 3974
|||||
Sbjct: 961 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 1020

Query: 3975 atgagcgcgaaaaacctttacggtcccccaggttcgggcgctccttgaggtgcccgagggga 4034
|||||
Sbjct: 1021 atgagcgcgaaaaacctttacggtcccccaggttcgggcgctccttgaggtgcccgagggga 1080

Query: 4035 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 4094
|||||
Sbjct: 1081 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1140

Query: 4095 aaccatttatcgcgtctgacattgacggcaaaagccgaccaaagattggccgtagcgtggca 4154
|||||
Sbjct: 1141 aaccatttatcgcgtctgacattgacggcaaaagccgaccaaagattggccgtagcgtggca 1200

Query: 4155 agtgtactataggctgggaagtgaagacgacccaacccgtgccaggcgcgagctggcg 4214
|||||
Sbjct: 1201 agtgtactataggctgggaagtgaagacgacccaacccgtgccaggcgcgagctggcg 1260

Query: 4215 ggttccaaggtcggtcgagatgctcgcgagaggggcagcggaacgatatgccccctcc 4274
|||||
Sbjct: 1261 ggttccaaggtcggtcgagatgctcgcgagaggggcagcggaacgatatgccccctcc 1320

Query: 4275 ttcccagaagcggggcgatcacctacagtccacgttggtggagctgaaacgctctgct 4334
|||||
Sbjct: 1321 ttcccagaagcggggcgatcacctacagtccacgttggtggagctgaaacgctctgct 1380

Query: 4335 ggacgacaacaggacaacgatctgatgcctcagacttccggcgtttctgtcgggagaga 4394
|||||
Sbjct: 1381 ggacgacaacaggacaacgatctgatgcctcagacttccggcgtttctgtcgggagaga 1440

Query: 4395 ggcgtgcgtctggacgctgcaaacatcgaaaaactgttttagattttcgcgcaaaagta 4454
|||||
Sbjct: 1441 ggcgtgcgtctggacgctgcaaacatcgaaaaactgttttagattttcgcgcaaaagta 1500

Query: 4455 gggaaagtttgagttttgaggtatttcccgcaaatagtgtaaatactttcgtgaaaacg 4514
|||||
Sbjct: 1501 gggaaagtttgagttttgaggtatttcccgcaaatagtgtaaatactttcgtgaaaacg 1560

Query: 4515 atgtgcaatatagcggtaagactatgaaatacacgcgctggacaggctgcaaaaagcaacgg 4574
|||||
Sbjct: 1561 atgtgcaatatagcggtaagactatgaaatacacgcgctggacaggctgcaaaaagcaacgg 1620

Query: 4575 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaatttccggtaaaaaag 4634
|||||
Sbjct: 1621 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaatttccggtaaaaaag 1680

Query: 4635 atgaatctggggcgaatgggttatagatcctgcagaattgcacagagtgttctcctcccat 4694
|||||
Sbjct: 1681 atgaatctggggcgaatgggttatagatcctgcagaattgcacagagtgttctcctcccat 1740

Query: 4695 caaagaaatacacaccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacacatg 4754
|||||
Sbjct: 1741 caaagaaatacacaccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacacatg 1800

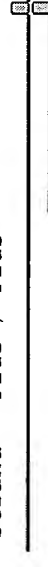
Query: 4755 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 4814
|||||
Sbjct: 1801 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 1860

Query: 4815 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtcttcaatttcat 4874
|||||
Sbjct: 1861 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtcttcaatttcat 1920

Query: 4875 caccgatgagagaggaagaccgccccctcaaaaacaaagatggtggaagatatcttgat 4934
|||||
Sbjct: 1921 caccgatgagagaggaagaccgccccctcaaaaacaaagatggtggaagatatcttgat 1980

Query: 4935 cctgggcttcaggagccttgcccttta 4960
|||||
Sbjct: 1981 cctgggcttcaggagccttgcccttta 2006

Score = 208 bits (108), Expect = 2e-49
Identities = 108/108 (100%)
Strand = Plus / Plus



Query: 5364 tactggcggaacacgcgatattgagcacagggccgcacttttagagcggaagcctata 5423
|||||
Sbjct: 2005 tactggcggaacacgcgatattgagcacagggccgcacttttagagcggaagcctata 2064

Query: 5424 acgagtaccacaaacactagaagccagattgaggaataagggaacgtg 5471

|||||
Sbjct: 2065 acgagtaccacaaacactagaaagccagattgaggaaaaatagggaacgtg 2112

CPU time: 0.05 user secs. 0.02 sys. secs 0.07 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 787
Number of extensions: 21
Number of successful extensions: 15
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 8509
Length of database: 12,527,565,053
Length adjustment: 28
Effective length of query: 8481
Effective length of database: 12,527,565,025
Effective search space: 106246278977025
Effective search space used: 106246278977025
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 23 (44.9 bits)